

European Association of Fish Pathologists



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# **Abstract Book**



#### 048-P

### Detection of Red-spotted grouper nervous necrosis virus (RGNNV) in shrimp and squid of the Mediterranean Sea

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The quest for sustainable fisheries and procurement of food supply has increased aquaculture production up to the world fisheries capture. Viral encephalopathy and retinopathy (VER), also known as viral nervous necrosis (VNN), is caused by nervous necrosis virus (NNV) and results in high mortality of larvae and juveniles of continuous increasing amount of fish species. The disease causes vacuolation and necrosis of the central nervous system.

The virus has a nude capsid protecting a bipartite RNA genome that consists of positive stranded molecules RNA1 and RNA2. Four NNV genotype strains distributed worldwide are discriminated according to sequence homology of the capsid protein encoded by RNA2. Preventive treatments prioritize the RGNNV (Redspotted grouper nervous necrosis virus) genotype that has the highest optimum temperature for replication and the broadest range of susceptible species. A flow of NNV between wild and cultured fish had been demonstrated, and reservoirs of NNV have been reported in invertebrates, raising concern on the spreading of NNV in the mariculture industry through contaminated food. The present study aimed to contribute in the surveillance of reservoirs of NNV in invertebrates of the unexplored western Mediterranean Sea.

We report the detection of the RGNNV strain in two species of squid (*Alloteuthis media* and *Abralia veranyi*), and in one shrimp (*Plesionika heterocarpus*) collected in 2015 in the Alboran Sea. According to RNA2 sequences obtained from invertebrates and reported to date in the Mediterranean Sea, the strain RGNNV is predominant in this semi-enclosed sea. Our results suggest that RGNNV distribution is apparently independent of host species and ecosystem, and similar between invertebrates and fish species that feed on invertebrates, calling for an increase in surveillance of NNV reservoirs in the wild.





#### 034-Р

### Immunological response of gilthead seabream during an outbreak of the parasite *Cryptocaryon irritans*

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*Cryptocaryon irritans*, a holotrichous ciliate protozoan, causes "marine white spot disease" and is frequent in commercial marine fish farms. It is considered to cause one of the most devastating parasitic diseases in aquaculture producing significant economic losses. This parasitosis mainly causes respiratory distress, disruption of lamellae structure, mucus hyperproduction and skin damage. *C. irritans* has low host-specificity and one of its susceptible species is gilthead seabream, which has an enormous importance in the aquaculture industry in the Mediterranean area.

In this work, we aimed to evaluate different parameters of the immune response of gilthead seabream during a natural outbreak with *C. irritans*. Diagnosis was carried out by visualization of the parasite in the gills, along with the presence of compatible disease signs. Two days after the appearance of fish mortalities due to *C. irritans*, fish were sampled. Serum was isolated and innate humoral immune responses including peroxidase, bactericidal, natural haemolytic complement or lysozyme activities analyzed. Gills and head-kidney were obtained to evaluate immune-relevant gene transcription by real-time PCR and for microscopical studies. The genes studied code for inflammatory proteins, leukocyte markers or antimicrobial peptides. Our Histopathological data confirmed the existence of the parasite in the gills and a heavy disruption of gills morphology. In serum, however, only the bactericidal activity was modified upon infection. The most altered genes were those related to inflammation.

This work is a first approach to determine the immune response triggered by this parasite in gilthead seabream and further research should be done to clarify the parasite-host interactions.





#### 014-P Shi drum (*Umbrina cirrosa*) juveniles are susceptible to all Nodavirus genotypes

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Nervous necrosis virus (NNV; family Nodaviridae, genus Betanodavirus) is the causative agent of viral retinopathy and encephalopathy (VER) disease, which mainly affects the larval and juvenile stages of fish. The virus has an acute lethal effect in larval stages and juveniles. According to the RNA2 sequence, NNV are mainly divided into four genotypes: RGNNV, SJNNV, BFNNV and TPNNV.

The shi drum (*Umbrina cirrosa*) is a serious candidate for the diversification of Mediterranean aquaculture. Although aspects related to nutrition or reproduction have been elucidated others related to pathology or immunity have been poorly studied. In this regard, the shi drum is a susceptible species for betanodavirus (RGNNV) infection, as several natural outbreaks have been reported. In order to expand the actual knowledge and understand the shi drum-NNV interactions we evaluated whether this fish species is susceptible to all the NNV genotypes.

Our data demonstrate that the laboratory infections with all the NNV genotypes produced clinical signs of the VER disease and mortalities in shi drum juveniles. Interestingly, clinical signs and histopathological lesions in the brain and retina were different depending on the genotype used. Finally, viral capsid protein was immunodetected in the brain and retina from all infected fish whilst infective particles were only recovered from RGNNV-, BFNNV- and TPNNV-infected specimens.

In conclusion, this work demonstrates that shi drum juveniles are susceptible to all four genotypes of NNV and represent the first step in studying host–NNV interactions and immune responses in this species, which should be further characterized.





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